

Fig. 1.

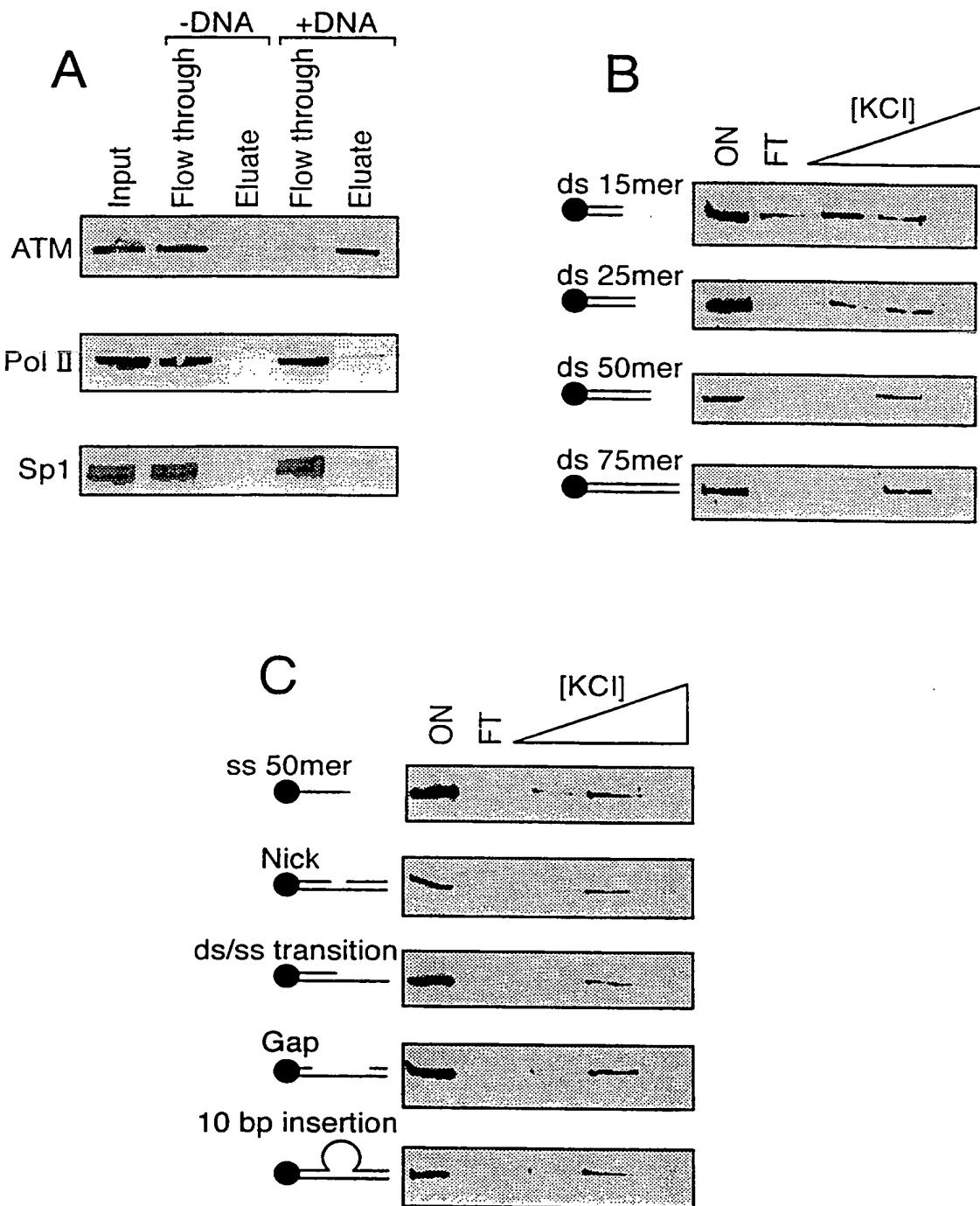


Fig.2.

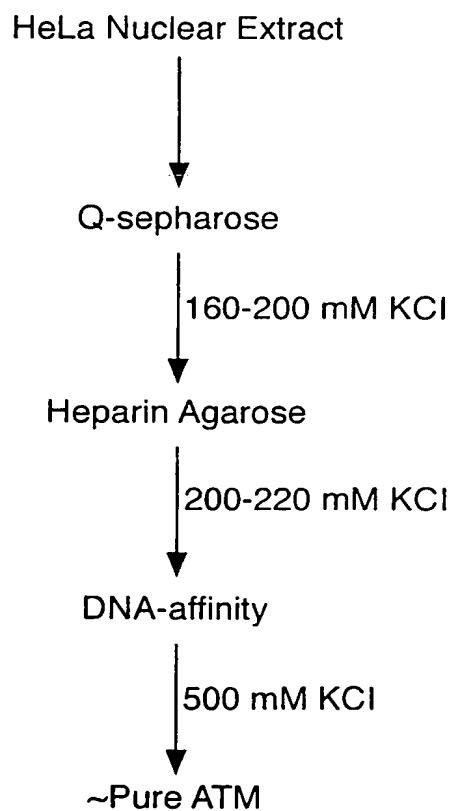
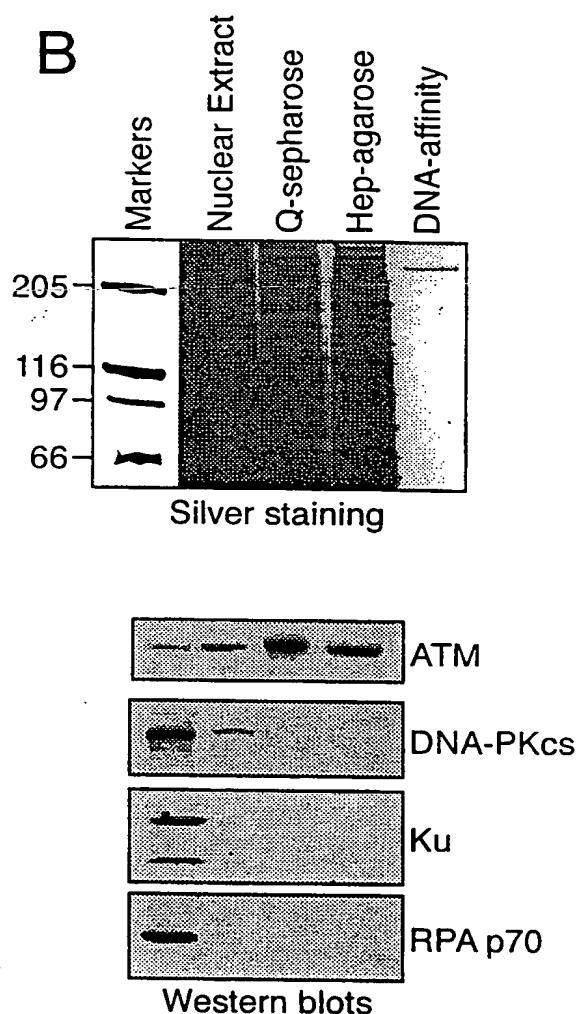
A**B**

Fig.3.

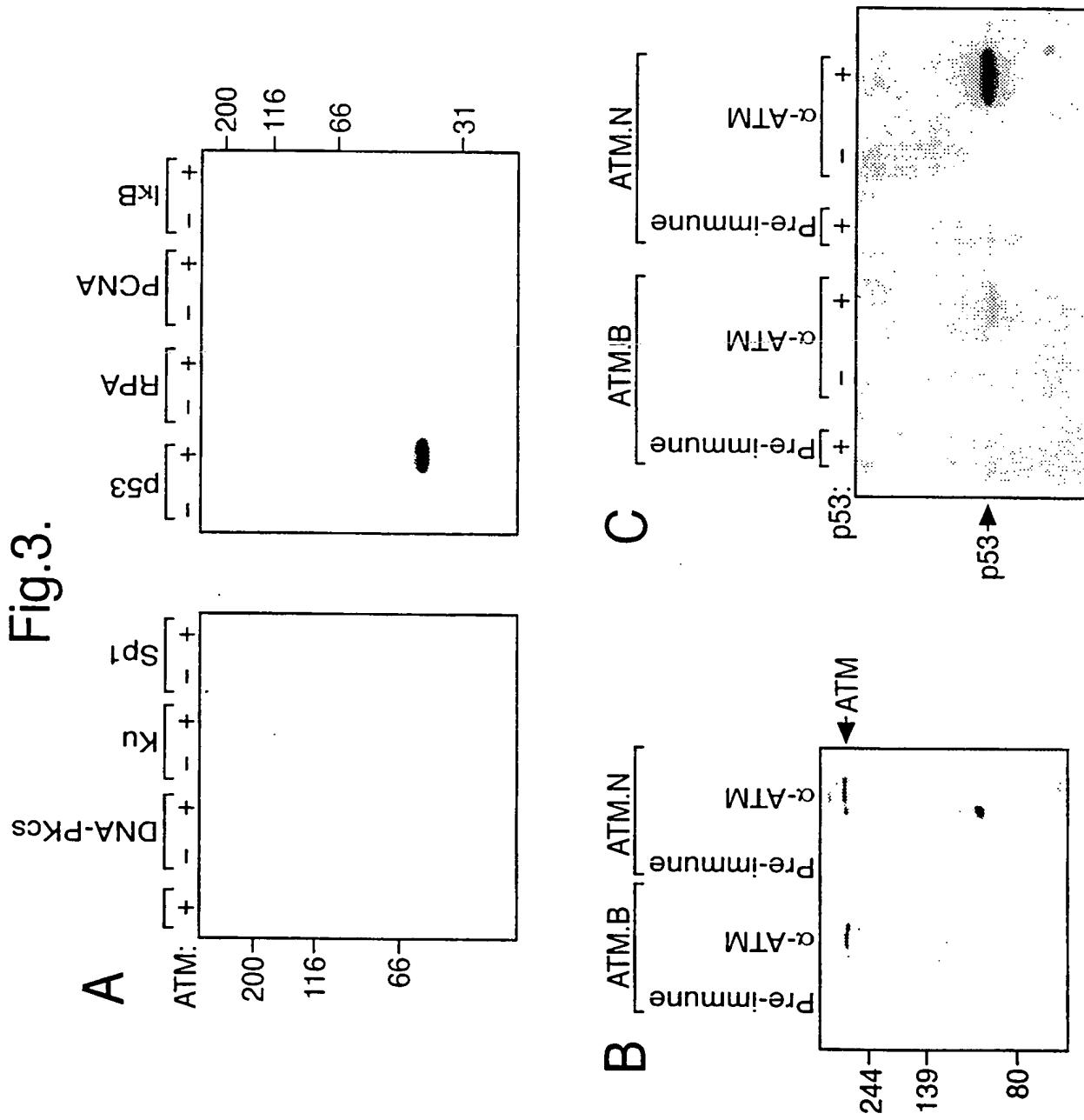


Fig.4.

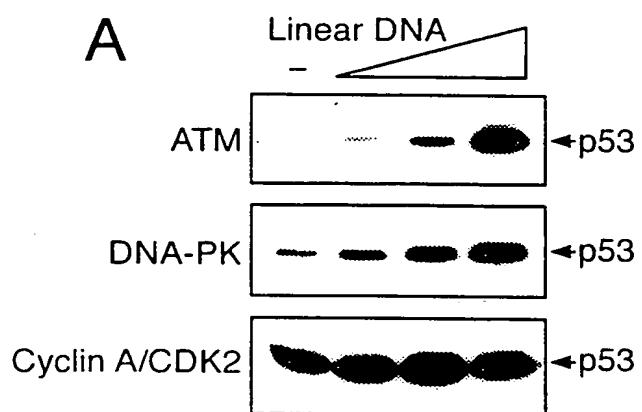
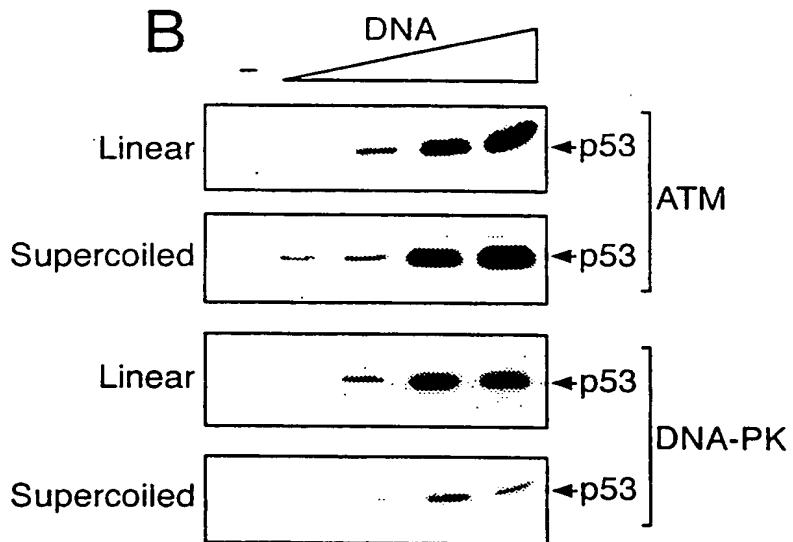
A**B**

Fig.5.

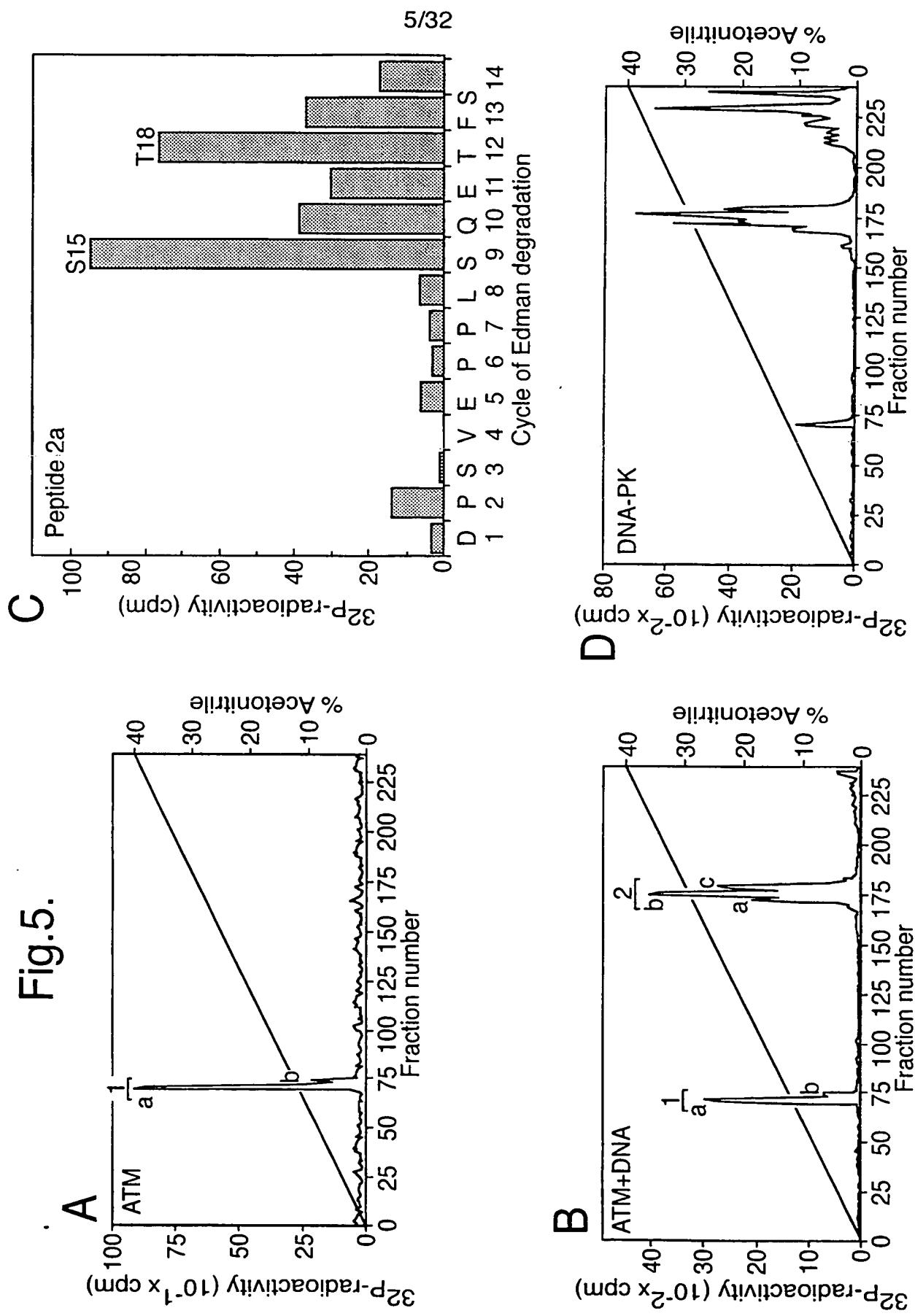


Figure 6a

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Figure 6b (1)

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Figure 6b (ii)

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Figure 6 b (iii)

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 2601 GCGATTGTTA ACATCAAAGC TAATGAATGA CATTGAGAT ATTTGTAAAA
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Figure 6b (iv)

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 5051 TGGAACTACA TAAAGATCAG ATGGTGGACA TTATGAGAGC TTCTCAGGAT
 5101 AATCCGCAAG ATGGGATTAT GGTGAAACTA GTGTCAATT GTTGTGAGTT
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Figure 6b (v)

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Figure 6b (v1)

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Figure 6b (vii)

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Figure 7a

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FH
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RRTEENLRKKGEPEHLLPPGSTKRALPNNTSSSPOPKKKPLDGEYFTLQIRGRERFEM
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XX
SQ  Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 other;

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M14695 Length: 1303 July 10, 1998 12:29 Type: N Check: 4902 ..

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1  GTCCAGGAGC AGGTAGCTGC TGGGCTCCGG GGACACTTIG CGTTCCGGGCT
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101 ACTGCCCTCC GGGTCACTGCATGGAGGAG CGGCAGTCAG ATCCTAGCGT
151 CGAGCCCCCT CTGAGTCAGG AAACATTTC AGACCTATGG AAACTACTTC
201 CTGAAAACAA CGTTCTGTCC CCCTTGCCGT CCCAAGCAAT GGATGATTG
251 ATGCTGTCCC CGGACGATAT TGAACAATGG TTCACTGAAG ACCCAGGTCC

```

Figure 7b (i)

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Figure 7b (11)

301 AGATGAAGCT CCCAGAAATGC CAGAGGCTGC TCCCCCGTG GCCCCTGCAC
351 CAGCGACTCC TACACCGGCG GCCCCTGCAC CAGCCCCCTC CTGGCCCCCTG
401 TCATCTTCTG TCCCTTCCCCA GAAAACCTAC CAGGGCAGCT ACGGTTTCCG
451 TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT
501 CCCCTGCCCT CAACAAGATG TTTTGCAAC TGGCCAAGAC CTGCCCTGTG
551 CAGCTGTGGG TTGATTCCAC ACCCCCCCCC GGCAACCGCG TCCGGCCCAT
601 GGCCATCTAC AAGCAGTCAC AGCACATGAC GGAGGTTGTG AGGCGCTGCC
651 CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC TCCTCAGCAT
701 CTTATCCGAG TGGAACGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA
751 CACTTTTGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT
801 CTGACTGTAC CACCATCCAC TACAACCTACA TGTTGTAACAG TTCCCTGCATG
851 GGCGGCATGA ACCGGAGGCC CATCCTCACC ATCATCACAC TGGAAGACTC
901 CAGTGGTAAT CTACTGGGAC GGAACAGCTT TGAGGTGCGT GTTTGTGCCT
951 GTCCCTGGGAG AGACCGGCCG ACAGAGGAAG AGAATCTCCG CAAGAAAGGG
1001 GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA
1051 CAACACCAAGC TCCTCTCCCC AGCCAAAGAA GAAACCACIG GATGGAGAAT
1101 ATTTCACCCCT TCAGATCCGT GGGCGTGAGC GCTTCGAGAT GTTCCGAGAG
1151 CTGAATGAGG CCTTGGAACCT CAAGGATGCC CAGGCTGGGA AGGAGCCAGG
1201 GGGGAGCAGG GCTCACTCCA GCCACCTGAA GTCCAAAAG GGTCAAGTCTA
1251 CCTCCCCGCCA TAAAAAAACTC ATGTTCAAGA CAGAAGGGCC TGACTCAGAC
1301 TGA

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Figure 8a (i)

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ID HS498441 standard; RNA; HUM; 8210 BP.
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AC U49844;
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DT 20-MAY-1996 (Rel. 47, Last updated, Version 1)
XX
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XX
KW
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-8210
RA Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L. ;
RT "cDNA cloning and gene mapping of a candidate human cell cycle
checkpoint protein";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2850-2855(1996).
XX
RN [2]
RP 1-8210
RA Cimprich K.A., Shin T.B., Keith C.T., Schreiber S.L. ;
RT ;
RL Submitted (22-FEB-1996) to the EMBL/GenBank/DDBJ databases.
RL Karlene A. Cimprich, Chemistry, Harvard University, 12 Oxford Street,
RL Cambridge, MA 02138, USA
XX
DR SPTREMBL; Q13535; Q13535.
XX
FH Key Location/Qualifiers
FH
FT source 1. .8210
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FT /chromosome="3"
FT /cell_type="Jurkat T-cell"
FT /map="3q22-q24"
FT CDS 106. .8040
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FT /db_xref="SPTREMBL:Q13535"
FT /note="similar to FRAP, Meclp, Tor1p, Tor2p, and ATM"
FT /gené="FRP1" or ATK
FT /product="FRAP-related protein"
FT /translation="MGEHGPLELASMIPALRELGSATPEEYNTVVQKPRQILCQFIDRIL
FT TDVNVAVELVKKTDSQPTSVMLDFIQHIMKSSPLMFVNVSHEAKGSCIEFSNWII
FT TRLLRIAATPSCHLLHKKICEVICSLFLFKSKSPAIFGVLTKEQLQLFEDLVYLHRRN
FT VMGHAVEWPVVMRSRFLSQLDEHMGYLQSAPLQLMSMQNLEFIEVILLMVLTRIIAIVFF
FT RRQEPLLWQIGCVLLEYGSPKIKSLAISFLTELQIQLPAQPASTFFESSFLELLKHLL
FT EMDITDQLKLYEEPLSKLTKLTFPFEAEAYRNIEPVYLNMLLEKLCVMFEDGVLMRLKSD
FT LLKAALCHLLQYFLKFVPGYESALQVRKVYVRNICKALLDVLGIEVDAYLLGPYAA
FT LKMESMEIIIEIQCQTQQENLSSNSDGISPKRRLRSSLNPSPKRAPKQTEELKHVDMNO
FT KSILWSALKOKAESLQIISLEYSGLKNPVIEMLEGIAVVLQLTALCTVHCSSHQNMNCRTF
FT KDCQHKSKKKPSSVVTWMSLDFYTJKVLKSCRSLLESVQKLDLEATIDKVKKIYDALIYM
FT QVNSSFEDHILEDLCGMLSLPWIYSHSDDGCLKLTTFAANLLTLSCRJSDSYSPQAQSR
FT CVFLLTLPRIFILEWRATAVYNWALQSSHEVIRASCVSGFFILLQQONSCNRVPKILID
FT KVKKDDSDIVKFKASFASLGQLVCLTHGMFYLTSSLTEPFSEHGVDLFCRNLKATSQHEC
FT SSSQLKASVCKPFLFLKKKIPSPVVKLAFIDNLHHLCKHLDFREDETDVKAVALGTLLNL
FT MEDPKDKDVRVAFSGNIKHIKLESLDSEDGFIKEFLVLRMKEAYTHAQISRNNEKDILIL
FT TTGDIGRAAKGDLVPFALLHLLHCLLSKSASVSGAAYTEIRALVAAKSVKLQSFFSQYK
FT KPIQFLVESLHSSQMTALPNTPCQNAQDVRKQDVAHQREMALNLSEIANVFDFPDLNR
FT FLTRTLQVLLPDLAAKASPAASALIRTGKQLNVNREILINNFKYTFSHLVCSCSKDE

```

Figure 8a (ii)

FT LERALHYLKNETEIELGSLLRQDFQGLHNELLRIGEHYQOVFNGLSILASFASDDPY
 FT QGPRDIISPELMADYLQPKLGLILAFFNMQLLSSVGIEDKKMNLNSLMSLMKLMGPKH
 FT VSSVRVKMMMTTLRTGLRFKDDFPELCCRAWDCFVRCLDHAICLGSLLSHVIVALLPLIHI
 FT QPKETAAIFHYLIENRDAVQDFLHEIYFLPDHPELKKIKAVLQEYRKETSESTDQLQTT
 FT LQLSMKAIQHENDVDRVIHALTSLKETLYKNQEKLKYATDSETVEPIISQLVTULLKGC
 FT QDANSQARLLCGECLGELGAIDPGRLDFSTTEIQGKDFTVTGVEDSSFAYGLLMELTR
 FT AYLAYADNSRAQDSAAYAIQELLSIYDCREMETNGPGHQLWRRFPEHVREILEPHLNTR
 FT YKSSQKSTDWSGVKKPIYLSKLGNSNFAEWASAWAGYLITKVRHDLASKIFTCCSIMMKH
 FT DFKVTIYLLPHILVVYVLLGCNQEDQQEVVAEIMAVLKHDQHTINTODIASDLCQLSTO
 FT TVFSMLDHLTOWARHKFQALKAEKCPHSKSNRNVDSMVSTVDYEDYQSUTRFLDLIPQ
 FT DTLAVASFRSKAYTRVMHESITEKKQNIQEHLGFLQKLKYAAMHEPDGVAGVSAIRK
 FT AEPSLKEQILEHESLGLLRDATAKYDRAIQLEPDQIHYHGUVKSMLGLGQLSTVITQV
 FT NGVHANRSEWTDELNTYRVEAAWKLSQLDVLVENYLAADGKSTTWSVRLGQLLSAKKRD
 FT ITAFYDSLKLVRRAEQIVPLSAASFERGSYQRGYEYIVRLHMLCELEHSIKPLFQHSPGD
 FT SSQEDSLNWWARLEMQTNSYRAKEPILALRALLSLNKRPDYNEMVGECWLQSAVARAK
 FT AGHHQTAYNALLNAGESRLAELYVERAKWLWSKGDVHQALIVLQKGVELCFPENETPPE
 FT GKNMLIHGRAMLLVGRFMEETANFESNAIMKKYKDVTACLPEDGHHFYLAKYYDKLMP
 FT MVTDNKMEKQGDLIRYIVLHFGRSLQYGNQFYQSMPRMLTLWLDYGTKEYWEKAGRS
 FT DRVQMRNDLGKINKVITEHTNLYAPLQFLTAFSQLISRICHSHDEVFVVLNEIIAKVFL
 FT AYPQQAMMMTAVKSSYPMRVNRCKEILNKAJHMKSKLEKFVGDATRLTDKLLCNCNK
 FT PVDGSSSTLSMSTHFKMLKKLVEEATFSEIILIPLOQSVMIPTLPSILGTHANASHEPFP
 FT GHWAYLAGFDDMVEILASLQPKKKISLKGSDGKFYIMMCKPKDDLRCRCLMEFNSLIN
 FT KCLRDAESRRRELHIRTYAVIPLNDECGIEIEWVNNTAGLRPILTKYKEKGVYMTGKE
 FT LRQCMLPKSAALSEKLKVFRFLLPRHPPIFHWFRLTFPDPTSWYSSRSAYCRSTAVM
 FT SMVGYILGLGDRHGENILFDSLGTGECHVDFNCLFNKGTFEVPEIVPFRLTHNMVNMG
 FT GPMGTEGLFRRACEVIMRLMRDQREPLMSVLKTFLHDPLVIEWSKPVKGHSKAPLNETGE
 FT VVNEKAKTHVLDIEQRLLQGVIKTRNRVTGLPLSIEGHVHYLIQEATDENLLCQMYLGWT
 PYM"
 XX

SQ Sequence 8210 BP; 2511 A; 1555 C; 1738 G; 2406 T; 0 other;

U49844 Length: 8210 July 10, 1998 12:08 Type: N Check: 4511 ..

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1 GCCTCCACAC GGCTCCGTCG GGGGCCGCGC TCTTCCGGCA GCGGTAGCTT
51 TGGAGACGCC GGGAACCGCGC GTTGGCGTGG TTGACTAGTG CCTCGCAGCC
101 TCAGCATGGG GGAACATGGC CTGGAGCTGG CTTCCATGAT CCCCCGCCCCG
151 CGGGAGCTGG GCAGTGCCAC ACCAGAGGAA TATAATACAG TTGTACAGAA
201 GCCAAGACAA ATTCTGTGTC AATTCAATGA CCGGATACTT ACAGATGTAA
251 ATGTTGTTGC TGTAGAACTT GTAAAGAAAA CTGACTCTCA GCCAACCTCC
301 GTGATGTTGC TTGATTTCAT CCAGCATATC ATGAATTCTT CCCCCACTTAT
351 GTTGTAAAT GTGAGTGGAA CCCATGAGGC CAAAGGCAGT TGTATTGAAT
401 TCAGTAATTG GATCATAACG AGACTCTGC GGATTCGAGC AACTCCCTCC
451 TGTCAATTGT TACACAAGAA AATCTGTGAA GTCATCTGTT CATTATTATT
501 TCTTTTTAAA AGCAAGAGTC CTGCTATTTT TGGGGTACTC ACAAAAGAAT
551 TATTACAATC TTTTGAAGAC TTGGTTTACC TCCATAGAAG AAATGTGATG
601 GGTCACTGTC TGGAATGGCC AGTGGTCATG AGCCGATTTT TAAGTCATT
651 AGATGAACAC ATGGGATATT TACAATCAGC TCCATTGAGC TTGATGAGTA
701 TGCAAAATTG AGAATTATT GAAGTCACTT TATTAATGGT TCTTACTCGT
751 ATTATTCGCAA TTGTGTTTT TAGAAGGCAA GAACTCTTAC TTTGGCAGAT
801 AGGTTGTTGTCTGCTAGAGT ATGGTAGTCC AAAAATTAAA TCCCTAGCAA

```

Figure 8b (i)

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Figure 8b (ii)

851 TTAGCTTTT AACAGAACCTT TTTCAGCTTG GAGGACTACC AGCACAAACCA
901 GCTAGCACTT TTTTCAGCTC ATTTTGGAA TTATTAAAAC ACCTTGTAGA
951 AATGGATACT GACCAATTGA AACTCTATGA AGAGCCATTA TCAAAGCTGA
1001 TAAAGACACT ATTTCCCTTT GAAGCAGAAG CTTATAGAAA TATTGAACCT
1051 GTCTATTAA ATATGCTGCT GGAAAAACTC TGTGTATGT TTGAAGACGG
1101 TGTGCTCATG CGGCTTAAGT CTGATTGCT AAAAGCAGCT TTGTGCCATT
1151 TACTGCAGTA TTTCTTAA TTTGTGCCAG CTGGGTATGA ATCTGCTTTA
1201 CAAGTCAGGA AGGTCTATGT GAGAAATATT TGTAAAGCTC TTTTGGATGT
1251 GCTTGGAAATT GAGGTAGATG CAGAGTACTT GTTGGGCCCA CTTTATGCAG
1301 CTTTGAAAAT GGAAAGTATG GAAATCATTG AGGAGATTCA ATGCCAAACT
1351 CAACAGGAAA ACCTCAGCAG TAATAGTGAT GGAATATGAC CAAAAGGCG
1401 TCGTCTCAGC TCGTCTCTAA ACCCTCTAA AAGAGCACCA AAACAGACTG
1451 AGGAAATTAA ACATGTGGAC ATGAACAAA AGAGCATATT ATGGAGTGCA
1501 CTGAAACAGA AAGCTGAATC CCTTCAGATT TCCCTTGAAT ACAGTGGCCT
1551 AAAGAATCCT GTTATTGAGA TGTTAGAAGG AATTGCTGTT GTCTTACAAC
1601 TGACTGCTCT GTGTACTGTT CATTGCTCTC ATCAAAACAT GAACTGCCGT
1651 ACTTTCAAGG ACTGTCAACA TAAATCCAAG AAGAAACCTT CTGTAGTGAT
1701 AACTTGGATG TCATTGGATT TTTACACAAA AGTGCTTAAG AGCTGTAGAA
1751 GTTTGTTAGA ATCTGTTCAAG AAACGTGGACC TGGAGGCAAC CATTGATAAG
1801 GTGGTGAAAA TTTATGATGC TTTGATTTAT ATGCAAGTAA ACAGTTCTATT
1851 TGAAGATCAT ATCCTGGAAG ATTTATGTGG TATGCTCTCA CTTCCATGGA
1901 TTTATTCCCA TTCTGATGAT GGCTGTTAA AGTTGACCAC ATTTGCCGCT
1951 AATCTCTAA CATTAAAGCTG TAGGATTTCA GATAGCTATT CACCACAGGC
2001 ACAATCACGA TGTGTGTTTC TTCTGACTCT GTTCCAAGA AGAATATTCC
2051 TTGAGTGGAG AACAGCAGTT TACAACGTGG CCCTGCAGAG CTCCCATGAA
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2151 GAATTCTGT AACAGAGTTTC CCAAGATTCT TATAGATAAA GTCAAAGATG
2201 ATTCTGACAT TGTCAAGAAA GAATTGCTT CTATACTTGG TCAACTTGTC
2251 TGTACTCTTC ACGGCATGTT TTATCTGACA AGTTCTTAA CAGAACCTTT
2301 CTCTGAACAC GGACATGTGG ACCTCTCTG TAGGAACCTG AAAGCCACCTT
2351 CTCAACATGA ATGTTCATCT TCTCAACTAA AAGCTTCTGT CTGCAAGCCA
2401 TTCCCTTTC TACTGAAAAA AAAAATACCT AGTCCAGTAA AACTTGCCTTT
2451 CATAGATAAT CTACATCATC TTTGTAAGCA TCTTGATTTT AGAGAAGATG
2501 AAACAGATGT AAAAGCAGTT CTTGGAACCTT TATTAATTTT AATGGAAGAT

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Figure 8b (111)

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 2601 GGAATCCTTG GACTCTGAAG ATGGATTTAT AAAGGAGCTT TTTGTCTTAA
 2651 GAATGAAGGA AGCATATACA CATGCCAAA TATCAAGAAA TAATGAGCTG
 2701 AAGGATACCT TGATTCTTAC AACAGGGGAT ATTGGAAGGG CCGAAAAGG
 2751 AGATTTGGTA CCATTTGCAC TCTTACACTT ATTGCATTGT TTGTTATCCA
 2801 AGTCAGCATC TGTCTCTGGA GCACCATACA CAGAAATTAG AGCTCTGGTT
 2851 GCAGCTAAAA GTGTTAAACT GCAAAGTTT TTCAGCCAGT ATAAGAAACC
 2901 CATCTGTCAG TTTTIGGTAG AATCCCTTCA CTCTAGTCAG ATGACAGCAC
 2951 TTCCGAATAC TCCATGCCAG AATGCTGACG TGCGAAAACA AGATGTGGCT
 3001 CACCAGAGAG AAATGGCTTT AAATACGTTG TCTGAAATTG CCAACGTTT
 3051 CGACTTTCCCT GATCTTAATC GTTTCTTAC TAGGACATTA CAAGTTCTAC
 3101 TACCTGATCT TGCTGCCAAA GCAAGCCCTG CAGCTCTGC TCTCATTGGA
 3151 ACTTTAGGAA ACAATTAAA TGTCAACGT AGAGAGATT TAATAAACAA
 3201 CTTCAAATAT ATTTTTCTC ATTTGGTCTG TTCTTGTCC AAAGATGAAT
 3251 TAGAACGTGC CCTTCATTAT CTGAAGAATG AAACAGAAAT TGAACGGGG
 3301 AGCCTGTTGA GACAAGATT CCAAGGATTG CATAATGAAT TATTGCTGCG
 3351 TATTGGAGAA CACTATCAAC AGGTTTTAA TGGTTGTCA ATACTTGCCT
 3401 CATTTCGCATC CAGTGATGAT CCATATCAGG GCCCCGAGAGA TATCATATCA
 3451 CCTGAACGTGA TGGCTGATTA TTACAAACCC AAATTGTTGG GCATTTGGC
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 3551 AAATGGCCCTT GAACAGTTTG ATGCTTTGTA TGAAGTTAAT GGGACCCAAA
 3601 CATGTCAGTT CTGTGAGGGT GAAGATGATG ACCACACTGA GAACTGGCCT
 3651 TCGATTCAAG GATGATTTC CTGAATTGIG TTGCAGAGCT TGGGACTGCT
 3701 TTGTTCGCTG CCTGGATCAT GCTTGTCTGG GCTCCCTCT CAGTCATGTA
 3751 ATAGTAGCTT TGTTACCTCT TATACACATC CAGCCTAAAG AAACGTGAGC
 3801 TATCTTCCAC TACCTCATAA TTGAAAACAG GGATGCTGTG CAAGATTTTC
 3851 TTICATGAAAT ATATTTTTA CCTGATCATC CAGAATTAAA AAAGATAAAA
 3901 GCCGTTCTCC AGGAATACAG AAAGGAGACC TCTGAGAGCA CTGATCTTCA
 3951 GACAACCTTT CAGCTCTCTA TGAAGGCCAT TCAACATGAA AATGTCGATG
 4001 TTICGTATTCA TGCTCTTACA AGCTTGAAGG AAACCTTGTG TAAAAATCAG
 4051 GAAAAACTGTA TAAAGTATGC AACAGACAGT GAAACAGTAG AACCTATTAT
 4101 CTCACAGTTG GTGACAGTGC TTTTGAAGG TTGCCAAGAT GCAAACCTCTC
 4151 AAGCTCGGTT GCTCTGTGGG GAATGTTAG GGGAAATTGGG GGCGATAGAT

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Figure 8b (iv)

4201 CCAGGTCGAT TAGATTTCTC AACAACTGAA ACTCAAGGAA AAGATTTAC
4251 ATTTGTGACT GGAGTAGAAG ATTCAAGCTT TGCCTATGGA TTATATGATGG
4301 AGCTAACAAAG AGCTTACCTT GCGTACGCTG ATAATAGCCG AGCTCAAGAT
4351 TCAGCTGCCT ATGCCATTCA GGAGTTGCTT TCTATTTATG ACTGTAGAGA
4401 GATGGAGACC AACGGCCCAG GTCACCAATT GTGGAGGAGA TTTCCCTGAGC
4451 ATGTTGGGA AATACTAGAA CCTCATCTAA ATACCAGATA CAAGAGTTCT
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5201 AACCATCTCT AAAAGAACAG ATCCTTGAAC ATGAAAGCCT TGGCTTGCTG
5251 AGGGATGCCA CTGCTTGTAA TGACAGGGCT ATTCAAGCTAG AACCAGACCA
5301 GATCATTCAT TATCATGGTG TAGTAAAGTC CATGTTAGGT CTGGTCAGC
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5401 TGGACAGATG AATTAAACAC GTACAGAGTG GAAGCAGCTT GGAAATIGTC
5451 ACAGTGGAT TTGGTGGAAA ACTATTGGC AGCAGATGGA AAATCTACAA
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5601 ACCTCTTCA GCTGCAAGCT TTGAAAGAGG CTCTACCAA CGAGGATATG
5651 AATATATATGT GAGATTGCAC ATGTTATGTG AGTGGAGCA TAGCATAAA
5701 CCACCTTCC AGCATTCTCC AGGTGACAGT TCTCAAGAAG ATTCTCTAAA
5751 CTGGGTAGCT CGACTAGAAA TGACCCAGAA TTOCTACAGA GCCAAGGAGC
5801 CTATCCTGGC TCTCOGGAGG GCTTTACTAA GCCTCAACAA AAGACCAGAT
5851 TACAATGAAA TGGTTGGAGA ATGCTGGCTG CAGAGTGCAGA GGGTAGCTAG

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Figure 8b (v)

5901 AAAGGCTGGT CACCACCAAGA CAGCCTACAA TGCTCTCCCTT AATGCAGGGG
 5951 AATCACGACT CGCTGAAC TG TACGTGGAAA GGGCAAAGTG GCTCTGGTCC
 6001 AAGGGTGATG TTTCACCAGGC ACTAATTGTT CTTCAAAAAG GTGTTGAATT
 6051 ATGTTTTCCT GAAAATGAAA CCCCACCTGA GGGTAAGAAC ATGTTAATCC
 6101 ATGGTCGAGC TATGCTACTA GTGGGCCGAT TTATGGAAGA AACAGCTAAC
 6151 TTTGAAAGCA ATGCAATTAT GAAAAAATAT AAGGATGTGA CCGCGTGCCT
 6201 GCCAGAATGG GAGGATGGGC ATTTTTACCT TGCCAAGTAC TATGACAAAT
 6251 TGATGCCCAT GGTACAGAC AACAAAATGG AAAAGCAAGG TGATCTCATC
 6301 CGGTATATAG TTCTTCATTT TGGCAGATCT CTACAATATG GAAATCAGTT
 6351 CATATATCAG TCAATGCCAC GAATGTTAAC TCTATGGCTT GATTATGGTA
 6401 CAAAGGCATA TGAATGGAA AAAGCIGGCC GCTCCGATCG TGTACAAATG
 6451 AGGAATGATT TGGGTAAAAT AAACAAGGTT ATCACAGAGC ATACAAACTA
 6501 TTTAGCTCCA TATCAATT TT TGACTGCTTT TTCACAATTG ATCTCTCGAA
 6551 TTTGTCATTC TCACGATGAA GTTTTTGTTG TCTTGATGGA AATAATAGCC
 6601 AAAGTATTTTC TAGCCTATCC TCAACAAGCA ATGTGGATGA TGACAGCTGT
 6651 GTCAAAGTCA TCTTATCCC TGCGTGTGAA CAGATGCAAG GAAATCCTCA
 6701 ATAAAGCTAT TCATATGAAA AAATCCTTAG AGAAAGTTGT TGGAGATGCA
 6751 ACTCGCCTAA CAGATAAGCT TCTAGAATTG TGCAATAAAC CGGTTGATGG
 6801 AAGTAGTTCC ACATTAAGCA TGAGCACTCA TTTTAAAATG CTTAAAAGC
 6851 TGGTAGAAGA AGCAACATT AGTGAATCC TCATTCCCT ACAATCAGTC
 6901 ATGATACCTA CACTTCCATC AATTCTGGGT ACCCATGCTA ACCATGCTAG
 6951 CCATGAACCA TTTCTGGAC ATTGGGCTA TATTGAGGG TTTGATGATA
 7001 TGGTGGAAAT TCTTGCTCT CTTCAGAAAC CAAAGAAGAT TTCTTTAAAA
 7051 GGCTCAGATG GAAAGTTCTA CATCATGATG TGTAAGCCAA AAGATGACCT
 7101 GAGAAAGGAT TGTAGACTAA TGGAATTCAA TTCTTGATT AATAAGTGCT
 7151 TAAGAAAAGA TGCAGAGTCT CGTAGAAGAG AACTTCATAT TCGAACATAT
 7201 GCAGTTATTIC CACTAAATGA TGAATGTGGG ATTATTGAAT GGGTGAACAA
 7251 CACTGCTGGT TTGAGACCTA TTCTGACCAA ACTATATAAA GAAAAGGGAG
 7301 TGTATATGAC AGGAAAAGAA CTTCGCCAGT GTATGCTACC AAAGTCAGCA
 7351 GCTTTATCTG AAAAATCTAA AGTATTCCGA GAATTCTCC TGCCCAGGCA
 7401 TCCTCCTATT TTTCATGAGT GGTTCTGAG AACATTCCCT GATCCTACAT
 7451 CATGGTACAG TAGTAGATCA GCTTACTGCC GTTCCACTGC AGTAATGTCA
 7501 ATGGTTGGTT ATATTCTGGG GCTTGGAGAC CGTCATGGTG AAAATATTCT

Figure 8b (v1)

7551 CTTTGATTCT TTGACTGGTG AATGCGTACA TGTAGATTTA AATTGTCTTT
7601 TCAATAAGGG AGAAACCTTT GAAGTTCCAG AAATTGTGCC ATTTCGCCTG
7651 ACTCATATAA TGGTTAACGG AATGGGTCT ATGGGAACAG AGGGTCTTTT
7701 TCGAAGAGCA TGTGAAGTTA CAATGAGGCT GATGCGTGAT CAGCGAGAGC
7751 CTTTAATGAG TGTCTTAAG ACTTTCTAC ATGATCCTCT TGTGGAATGG
7801 AGTAAACCAG TGAAAGGGCA TTCCAAAGCG CCACTGAATG AAACTGGAGA
7851 AGTGTCAAT GAAAAGGCCA AGACCCATGT TCTTGACATT GAGCAGCGAC
7901 TACAAGGTGT AATCAAGACT CGAAAATAGAG TGACAGGACT GCCGTTATCT
7951 ATTGAAGGAC ATGTGCATTA CCTTATACAG GAAGCTACTG ATGAAAACCTT
8001 ACTATGCCAG ATGTATCTTG GTGGACTCC ATATAATGTGA AATGAAATTAA
8051 TGTAAAAGAA TATGTTAATA ATCTAAAAGT AATGCATTIG GTATGAATCT
8101 GTGGTGTAT CTGTTCAATT CTAAGTACA ACATAAATTT ACGTTCTCAG
8151 CAACTGTTAT TTCTCTCTGA TCATTAATTA TATGAAAAT AATATACATT
8201 CACTCGTGCC

Figure 9a (1)

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ID HS349941 standard; RNA; HUM; 12780 BP.
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AC U34994;
XX
NI g995940
XX
DT 26-SEP-1995 (Rel. 45, Created)
DT 22-FEB-1997 (Rel. 51, Last updated, Version 4)
XX
DE Human DNA-dependent protein kinase catalytic subunit (DNA-PKcs)
DE mRNA, complete cds.
XX
KW
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates;
OC Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-12780
RX MEDLINE: 95401275.
RA Hartley K.O., Gell D., Smith G.C., Zhang H., Divecha N., Connnelly M.A.,
RA Admon A., Lees-Miller S.P., Anderson C.W., Jackson S.P.,
→ RT "DNA-dependent protein kinase catalytic subunit: a relative of
RT phosphatidylinositol 3-kinase and the ataxia telangiectasia gene
RT product";
RL Cell 82:849-856(1995).
XX
RN [2]
RP 1-12780
RA Gell D. ;
RT ;
RL Submitted (29-AUG-1995) to the EMBL/GenBank/DDBJ databases.
RL Dave Gell, Zoology, Wellcome/CRC, Tennis Court Road, Cambridge CB2 1QR,
RL UK
XX
DR SPTREMBL; Q13327; Q13327.
XX
OC NCBI gi: 995940
XX
FH Key Location/Qualifiers
FH
FT source 1. .12780
FT /organism="Homo sapiens"
FT /chromosome="8"
FT /cell_type="He-La"
FT /map="8q11"
FT CDS 53. .12343
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FT /db_xref="PID:g995941"
FT /db_xref="SPTREMBL:Q13327"
FT /note="DNA-activated protein kinase catalytic subunit; PI
FT kinase family member; partial genomic sequence located in
FT GenBank Accession Number L27425; Method: conceptual
FT translation supplied by author. NCBI gi: 995941"
FT /gene="DNA-PKcs"
FT /product="DNA dependent protein kinase catalytic subunit"
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CLKGLSSLLCNPKMSMEEDPQTTSREIFNFVLKAIRPQIDLKRYAVPSAGLRLFALHASQ
FSTCLLDNYVSLFEVLLKWCANTVVELKKAALSALESFLKQVSNMVAKNAEMHKNKLOY
FMEQFYGIIRNVDSDNNKEELSIAIRGYGLFAGPCKVINAKDVFMYVELIQRCKQMFLTQ
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Figure 9 (ii)

FT KWKVPTYKDYVDLFRHLLSSDQMMDSI LADEAFFSVNSSSESLNHLLYDEFVKSVLKIV
 FT EKLDLTLEIQTGEOENGDEAPGVWMIPSDPAANLHPAKPKDFSAFINLVEFCREILP
 FT EKQAEFFEPWVYSFSYELILOSTRPLISGFYKLLSITVRNAKKIKYFEGVSPKSLKHS
 FT PEDPEKYSCFALFVFKFGKEAVKMKQYKDELLASCLTFLSLSPHNIIELDVRAYVPAQO
 FT MAFKLGLSYTPLAEVGLNALEEWSIYIDRHVMQPYYKDIILPCLDGYLKTSALSDETKN
 FT WEVSALSRAAQGFNKKVVLKHLKKTKNLSSNEAISLEEIRIRVVQMLGSLGGQINKNLL
 FT TVTSSDEMMKSYVAWDREKRRLSFAVPFREMCKPVIFLDVFLPRVTELALTASDRQTKVAA
 FT CELLHSMVMFMILGKATQMPPEGGQGAPPMYQLYKRTFPVLLRLACDVDQVTRQLYEPLVM
 FT QLIHWFTMNNKKFESQDTVSLEAILDGIVDPVDSLRLDFCGRCIREFLKWSIKQITPQQ
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 FT DLWKLLAHHCGRPQTECRHKSIELFYKVPLLPGNRSPLWLKDVLKEEGVSFLINTFE
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 FT FGGLCERLVSLLNPAVLSTASLGSSQGSVIFHSHGEYFYSLFSETINTELLKNLDLAV
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 FT LETKMAVLALLAKILQIDSFSNTSHGSFPEVFTTYISLLADTKLDLHLKGQAVTLLP
 FT FFTSLTGGSEELRRVLEOLIVAHFPMOSREFPPGTPRFMNVVDCMKKFLDALELSQSP
 FT MLLLEMTEVLCREQQHVMEELFQSSFRRIARRGSCVTQVGLIESVYEMFRKDDPRLSFT
 FT RQSFVDRSLLTLLWHCSLDALREFFSTIVVDAIDVLKSRFTKLNESTFDTQITKMGYY
 FT KILDVMSRLPKDDVHAKESKINQVFHGSCITEGENELTKTLIKLCYDAFTENMAGENQL
 FT LERRLYHCAAYNCAISVICCVFNLKFYQGFLFSEKPEKNLLIFENLIDLKRRYNFPV
 FT EVEVPMERKKYIEIRKEAREAANGSDGSPMSLSSYLADSTLSEEMSQFDFSTGVQS
 FT YSYSSQDPRPATGRFRRREQRDPVTVDVLELEMDELNRHECMAPLTALVHMHRSLGP
 FT PGEEDDSVPRDLPSWMKFLHGKLNPIVPLNIRFLAKLVINTEEVFRPYAKHWLSPLL
 FT QLAASENNGGEGIHYMVEIVATLISWTGLATPTGVPKDEVLANRLLNFLMKHVFHPKR
 FT AVFRHNLEIITLVECWKDCCLSIPYRLIFEKFSGKDPSKDNCSVGIQLLGIVMANDLPP
 FT YDPQCGIQSSEYFQALVNNMSFVRYKEVYAAAAEVGLILRYVMERKNILEESLCELVA
 FT KOLKQHQNTMEDKFIVCLNKVTKSFPPLAQDRFMNAVFFLPKFHGVLKTLCLEVVLCRV
 FT EGMTELYFQLKSKDFVQVMPHRDERQVKVCLDIIYKMMPLKPKVELRELLNPVVEFVSHP
 FT STTCREQMYNILMWIHNDYRDPESETDNDQSEIFKLAQDVLIQGLIDENPGLQLIIRNF
 FT WSHTTRLPSNTLDRLLALNSLYSPKIEVHFLSLATNFLLEMTPSMSPDYPNPMFEHPLSE
 FT CEFQEYTIQSDWRFRSTVLTQMFVETQASQGTIQTRTQEGSLSARWPVAGQIRATQQH
 FT DFTLTQTAQGRSSFDWLTSQSTDPLVQDHTSPSSDSSLFAHKRSERLQRAFLKSVGPDFG
 FT KKRLGLPGDEVDNKVKGAGRTDQLRLLLRFMRDQEKLSLMYARKGVAEQKREKEIKSE
 FT LKMKODAQVVLYRSYRHGDLFDIPIQIKHSSLITPLQAVAQRDPPIAKQLFSSLFSGILKE
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 FT EADQSLLTFIQKAMHGELOKAILEHYSQELSLLYLLQDDVDRAKYYTQNGIQSFMONY
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 FT DPMNIWDDIITNRCFFLSKIEEKLTPPEDNSMNVDQDGDPDSRMEVQEQQEEDISSLIR
 FT SCKFSMKMKMIDSARKQNNSFLAMKLLKELHKESTKTRDDWLWSVWQSYCRLSHCRSRSO
 FT GCSEQVLTVLKTVSLLDENNVSSYLNKXNLAFRDQNLILLGTTYRIIANALSSPACLAE
 FT IEEDKARRILELGSSSSEDKSVIAGLYQRAFOHLSAEVQAAAEEAQPPSWSCGPAAGV
 FT IDAYMTLADFCDOQLRKEEENASVTDQALQAYPALVVEKMLKALKLNSNEARLKFPRL
 FT LQIILERYPEETLSLMTKEISSVPCWQFISWISHMALLDKDQAVAVQHSVEEITDNYPQ
 FT AIVYPIIISSESYSFKDTSTGHKNEFVARIKSKLDQGGVIQDFINALDQLSNPELLFK
 FT DWSNDVRAEELAKTPVNNKNIKMYERMYAALGDPKAPGLGAFRRKFIQTFGKEFDKHF
 FT KGGSKLLRMKLSDFNDITRNLLMKMKDPSKPPGNLKECPMSDFKVEFLRNELEIPGQ
 FT YDGRGKPLPEYHVRIAGFDERTVMASLPRKRIITRGHDEREHPFLVKGGEDLRQDQR
 FT VEQLFQVMNGILAQDSACSORALQLRTYSVVPMTSSDPRAPPCEYKDWLTKMSGKHDVG
 FT AYMLMYKGANRTEITVTSFRKRESKVPADLLKRAFVRMSTSPEAFLALRSFASSHALLC
 FT ISHWILGIGDRHINNMVAMETGGVIGIDFGHAFGSATQFLPVPELMPFRLTRQFINLM
 FT LPMKETGLMYSIMHALRAFRSDPGLLINTMDVFKEPSFDWKNFEOQKMLKKGGSWIQE
 FT INVAEKNWYPRQKICYAKRKLAGANPAVITCDELLGHEKAPAFRDYVAVARGSKDHNI
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XX SQ Sequence 12780 BP; 3612 A; 2769 C; 3084 G; 3314 T; 1 other;

U34994 Length: 12780 July 10, 1998 12:15 Type: N Check: 8189 .. Figure 9b(1)

1 ATTTCCGGGT CGGGGCCGAG CGGGCGCACG CGGGGAGCG GGACTCGGCG

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Figure 9b (ii)

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 151 ACTGATCCGC GGCCCTGGGGC AGGAATGCGT CCTGAGCAGC AGCCCCGGG
 201 TGCTGGCATT ACAGACATCT TTAGTTTTT CCAGAGATTT CGGTTTGCTT
 251 GTATTITGTCC GGAAGTCACT CAACAGTATT GAATTTCTG AATGTAGAGA
 301 AGAAATCCTA AAGTTTTAT GTATTITCTT AGAAAAAAATG GGCCAGAAGA
 351 TCGCACCTTA CTCTGTTGAA ATTAAGAAC A CTTGTACCAG TGTGTTATACA
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 801 ATTTTGTACT AAAGGCAATT CGTCCTCAGA TTGATCTGAA GAGATATGCT
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 1301 GTTGCAAGCG TCTTGCTGTA CCTTGACACA GTTCCCTGAGG TGTATACTCC
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 1501 GCATCAGGGT TTAATCAGAA TATGTTCTAA ACCAGTGGTC CTTCCAAAGG
 1551 GCCCTGAGTC TGAATCTGAA GACCACCGTG CTCAGGGGA AGTCAGAACT
 1601 GGCAAATGGA AGGTGCCAC ATACAAAGAC TACGTGGATC TCTTCAGACA
 1651 TCTCCTGAGC TCTGACCAGA TGATGGATTIC TATTTTAGCA GATGAAGCAT

Figure 9b (iii)

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 1751 GAATTIGTAA AATCCGTTTT GAAGATTGTT GAGAAATTGG ATCTTACACT
 1801 TGAAATACAG ACTGTTGGGG AACAAAGAGAA TGGAGATGAG GCGCCTGGTG
 1851 TTTGGATGAT CCCAACCTCA GATCCAGCGG CTAACCTGCA TCCAGCTAAA
 1901 CCTAAAGATT TTTCGGCTTT CATTAAACCTG GTGGAATTG GCAGAGAGAT
 1951 TCTCCCTGAG AAACAAGCAG AATTTTTGAA ACCATGGGTG TACTCATTGTT
 2001 CATATGAATT AATTTTGCAA TCTACAAGGT TGCCCCCAT CAGTGGTTTC
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 2151 AGTATTCTTG CTTTGCTTTA TTTGTGAAAT TTGGCAAAGA GGTGGCAGTT
 2201 AAAATGAAGC AGTACAAAGA TGAACTTTG GCCTCTTGTT TGACCTTTCT
 2251 TCTGTCCTTG CCACACAAACA TCATTGAACG CGATGTTAGA GCCTACGTT
 2301 CTGCACTGCA GATGGCTTTC AAACTGGGCC TGAGCTATAC CCCCTGGCA
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Figure 9b (iv)

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3551 GATCTGGTCA AGTGGCTTTT AGCTCATTGT GGGAGGCCCG AGACAGAATG
3601 TCGACACAAA TCCATTGAAC TCTTTATAA ATTGTTCCCT TTATTGCCAG
3651 GCAACAGATC CCCTAATTTG TGGCTGAAAG ATGTTCTCAA GGAAGAAGGT
3701 GTCTCTTTTC TCATCAACAC CTGGAGGGGG GGTGGCTGTG GCCAGCCCTC
3751 GGGCATCCTG GCCCAGCCCA CCCTCTTGTA CCTTCGGGGG CCATTCAAGCC
3801 TGCAGGCCAC GCTATGCTGG CTGGACCTGC TCCTGGCCGC GTTGGAGTGC
3851 TACAACACGT TCATTGGCGA GAGAACIGTA GGAGCGCTCC AGGTCTAGG
3901 TACTGAAGCC CAGTCITTCAC TTTTGAAAGC AGTGGCTTTTC TTCTTAGAAA
3951 GCATTGCCAT GCATGACATT ATAGCAGCAG AAAAGTGCTT TGGCACTGGG
4001 GCAGCAGGTA ACAGAACAAAG CCCACAAGAG GGAGAAAGGT ACAACTACAG
4051 CAAATGCACC GTTGTGGTCC GGATTATGGA GTTACCAACG ACTCTGCTAA
4101 ACACCTCCCC GGAAGGATGG AAGCTCCTGA AGAAGGACTT GTGTAATACA
4151 CACCTGATGA GAGTCCTGGT GCAGACGCTG TGTGAGCCCG CAAGCATAGG
4201 TTTCAACATC GGAGACGTCC AGGTTATGGC TCATCTTCCT GATGTTTGTG
4251 TGAATCTGAT GAAAGCTCTA AAGATGTCCC CATACAAAGA TATCCTAGAG
4301 ACCCATCTGA GAGAGAAAAT AACAGCACAG AGCATTGAGG AGCTTTGTGC
4351 CGTCAACTTG TATGGCCCTG ACGOGCAAGT GGACAGGAGC AGGCTGGCTG
4401 CTGTTGTGTC TGCTGTAAA CAGCTTCACA GAGCTGGCT TCTGCATAAT
4451 ATATTACCGT CTCAGTCCAC AGATTTGCAT CATTCTGTTG GCACAGAACT
4501 TCTTTCCCTG GTTATATAAG GCATTGGCCC TGGAGATGAG AGACAGTGTG
4551 TGCCCTCTCT AGACCTCAGT TGTAAGCAGC TGGCCAGCGG ACTTCTGGAG
4601 TTAGCCTTTG CTTTGGAGG ACTGTGTGAG CGCCTTGTGA GTCTCTCCT
4651 GAACCCAGCG GTGCTGTCCA CGGCGTCCCT GGGCAGCTCA CAGGGCAGCG
4701 TCATCCACTT CTCCCCATGGG GAGTATTCT ATAGCTTGTGTT CTCAGAAACG
4751 ATCAACACGG AATTATTGAA AAATCTGGAT CTTGCTGTAT TGGAGCTCAT
4801 GCAGTCCTCA GTGGATAATA CCAAAATGGT GAGTGGCGTT TTGAACGGCA
4851 TGTTAGACCA GAGCTTCAGG GAGCGAGCAA ACCAGAAACA CCAAGGACTG
4901 AAACTTGCGA CTACAATTCT GCAACACTGG AAGAAAGTGTG ATTICATGGTG
4951 GGCCAAAGAT TCCCCCTCTCG AAACTAAAAT GGCAGTGCTG GCCTTACTGG
5001 CAAAAATTTC ACAGATTGAT TCATCTGTAT CTTTAATAC AAGTCATGGT

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Figure 9b (v)

5051 TCATTCCTG AAGTCTTAC AACATATATT AGTCTACTTG CTGACACAAA
 5101 GCTGGATCTA CATTAAAGG GCCAAGCTGT CACTCTTCCTT CCATTCTCA
 5151 CCAGCCTCAC TGGAGGCAGT CTGGAGGAAC TTAGACGTGT TCTGGAGCAG
 5201 CTCATCGTTG CTCACCTCCC CATGCAGTCC AGGGAATTTC CTCCAGGAAC
 5251 TCCGCGGTTTC AATAATTATG TGGACTGCAT GAAAAAGTTT CTAGATGCAT
 5301 TGGAATTATC TCAAAGCCCT ATGTTGTTGG AATTGATGAC AGAAGTTCTT
 5351 TGTGGGAAC AGCAGCATGT CATGGAAGAA TTATTTCAAT CCAGTTTCAG
 5401 GAGGATTGCC AGAAGGGGTT CATGTGTCAC ACAAGTAGGC CTTCTGGAAA
 5451 GCGTGTATGA AATGTTCAAGG AAGGATGACC CCCGCCTAACG TTTCACACCG
 5501 CAGTCCTTTCG TGGACCGCTC CCTCCTCACT CTGCTGTGGC ACTGTAGCCT
 5551 GGATGCTTTG AGAGAATTCT TCAGCACAAT TGTGGTGGAT GCCATTGATG
 5601 TGTGAAAGTC CAGGTTTACA AAGCTAAATG AATCTACCTT TGATACTCAA
 5651 ATCACCAAGA AGATGGGCTA CTATAAGATT CTAGACGTGA TGTATTCTCG
 5701 CCTTCCCCAAA GATGATGTTTC ATGCTAAGGA ATCAAAAATT AATCAAGTTT
 5751 TCCATGGCTC GTGTATTACA GAAGGAAATG AACTTACAAA GACATTGATT
 5801 AAATTGTCAC ACGATGCATT TACAGAGAAC ATGGCAGGAG AGAACATCAGCT
 5851 GCTGGAGAGG AGAAGACTTT ACCATTTGTC AGCATAAAC TGCGCCATAT
 5901 CTGTCATCTG CTGTCCTTC AATGAGTTAA AATTTTACCA AGGTTTCTG
 5951 TTTAGTGAAA AACCAAGAAAA GAACTTGCTT ATTTTGAAA ATCTGATCGA
 6001 CCTGAAGCGC CGCTATAATT TTCTGTAGA AGTTGAGGTT CCTATGGAAA
 6051 GAAAGAAAAA GTACATTGAA ATTAGGAAAG AAGCCAGAGA AGCAGCAAAT
 6101 GGGGATTTCAG ATGGTCCTTC CTATATGTCT TCCCTGTCAT ATTTGGCAGA
 6151 CAGTACCCCTG AGTGAGGAAA TGAGTCATT TGATTCTICA ACCGGAGTTTC
 6201 AGAGCTATTTC ATACAGCTCC CAAGACCTA GACCTGCCAC TGGTCGTTT
 6251 CGGAGACGGG AGCAGCGGG .CCCCACGGTG CATGATGATG TGCTGGAGCT
 6301 GGAGATGGAC GAGCTCAATC GGCATGAGTG CATGGGGGCC CTGACGGGCC
 6351 TGGTCAAGCA CATGCACAGA AGCCTGGGCC CGCCTCAAGG AGAAGAGGAT
 6401 TCAGTGCCAA GAGATCTTCC TTCTTGATG AAATTCCTCC ATGGCAAATC
 6451 GGGAAATCCA ATAGTACCAT TAAATATCCG TCTCTTCTTA GCCAAGCTTG
 6501 TTATTAATAC AGAAGAGGTC TTTCGCCCTT ACCGCGAAGCA CTGGCTTAGC
 6551 CCCTTGCTGC AGCTGGCTGC TTCTGAAAAC AATGGAGGAG AAGGAATTCA
 6601 CTACATGGTG GTTGAGATAG TGGCCACTAT TCTTTCATGG ACAGGCTTGG
 6651 CCACTCCAAC AGGGGTCCCT AAAGATGAAG TGTAGCAAA TCGATTGCTT
 6701 AATTTCTAA TGAAACATGT CTTTCATCCA AAAAGAGCTG TGTATTAGACA

Figure 9b (vi)

6751 CAACCTTGAA ATTATAAAGA CCCTTGTGCA GTGCTGGAAG GATTGTTTAT
 6801 CCATCCCTTA TAGGTTAATA TTTGAAAAGT TTTCCGGTAA AGATCCTAAT
 6851 TCTAAAGACA ACTCAGTAGG GATTCAATTG CTAGGCATCG TGATGGCAA
 6901 TGACCTGCCT CCCTATGACC CACAGTGTGG CATCCAGAGT AGCGAATACT
 6951 TCCAGGCTTT GGTGAATAAT ATGTCCTTIG TAAGATATAA AGAAGTGTAT
 7001 GCCGCTGCAG CAGAAGTTCT AGGACTTATA CTTCGATATG TTATGGAGAG
 7051 AAAAAACATA CTGGAGGAGT CTCTGTGTGA ACTGGTTGCG AAACAATTGA
 7101 AGCAACATCA GAATACTATG GAGGACAAGT TTATTGTGTG CTTGAACAAA
 7151 GTGACCAAGA GCTTCCCTCC TCTTGCAGAC AGGTTCATGA ATGCTGTGTT
 7201 CTTTCTGCTG CCAAAATTTC ATGGAGTGTG GAAAACACTC TGTCTGGAGG
 7251 TGGTACTTTG TCGTGTGGAG GGAATGACAG AGCTGTACTT CCAGTTAAAG
 7301 AGCAAGGACT TCGTTCAAGT CATGAGACAT AGAGATGAAA GACAAAAGT
 7351 ATGTTTGGAC ATAATTATA AGATGATGCC AAAGTTAAAA CCAGTAGAAC
 7401 TCCGAGAACT TCTGAACCCC GTTGTGGAAT TCGTTTCCCCA TCCTTCTACA
 7451 ACATGTAGGG AACAAATGTA TAATATTCTC ATGTGGATTG ATGATAATTA
 7501 CAGAGATCCA GAAAGTGAGA CAGATAATGA CTCCCAGGAA ATATTTAAGT
 7551 TGGCAAAAGA TGTGCTGATT CAAGGATTGA TCGATGAGAA CCCTGGACTT
 7601 CAATTAATTG TTGCAAATTCTG CTGGAGCCAT GAAACTAGGT TACCTTCAAA
 7651 TACCTTGGAC CGGTTGCTGG CACTAAATTTC TTATATTCTC CCTAAGATAG
 7701 AAGTGCACTT TTTAAGTTTA GCAACAAATT TTCTGCTGCA AATGACCAGC
 7751 ATGAGCCCAG ATTATCCAAA CCCCATGTTTC GAGCATCCTC TGTCAAGATG
 7801 CGAATTTCAG GAATATACCA TTGATTCTGA TTGGCGTTTC CGAAGTACTG
 7851 TTCTCACTCC GATGTTTGTG GAGACCCAGG CCTCCCCAGGG CACTCTCCAG
 7901 ACCCGTACCC AGGAAGGGTC CCTCTCAGCT CGCTGGCCAG TGGCAGGGCA
 7951 GATAAGGCC ACCCAGCAGC AGCATGACTT CACACTGACA CAGACTGCAG
 8001 ATGGAAGAAG CTCATTTGAT TGGCTGACCG GGAGCAGCAC TGACCOOGCTG
 8051 GTGACCCACA CCAGTCCCTC ATCTGACTCC TTGCTGTTTG CCCACAAGAG
 8101 GAGTCAAAGG TTACAGAGAG CACCCCTGAA GTCACTGGGG CCTGATTTTG
 8151 GGAAAAAAAG GCTGGGCCTT CCAGGGACCG AGGTGGATAA CAAAGTGAAGA
 8201 GGTGCGGCCG GCCGGACGGA CCTACTACGA CTGCGCAGAC GGTTTATGAG
 8251 GGACCAAGGAG AAGCTCAGTT TGATGTATGC CAGAAAAGGC GTTGCTGAGC
 8301 AAAAACGAGA GAAGGAAATC AAGAGTGTGAGT TAAAAATGAA GCAGGATGCC
 8351 CAGGTOGTTC TGTACAGAAG CTACCGGCAC GGAGACCTTC CTGACATCA

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Figure 9b (vii)

8401 GATCAAGCAC AGCAGCCTCA TCACCCCGTT ACAGGCCGTG GCCCAGAGGG
 8451 ACCAATAAT TGCAAAACAG CTCTTGTAGCA GCTTGTTTC TGGAATTTCG
 8501 AAAGAGATGG ATAAATTAA GACACTGTCT GAAAAAAACA ACATCACTCA
 8551 AAAGTTGCTT CAAGACTICA ATCGTTTCT TAATACCACC TTCTCTTCT
 8601 TTCCACCCCTT TGTCTCTTGT ATTCAAGGACA TTAGCTGTCA GCACGCAGCC
 8651 CTGCTGAGCC TCGACCCAGC GGCTGTTAGC GCTGGTTGCC TGGCCAGCCT
 8701 ACAGCAGCCC GTGGGCATCC GCCTGCTAGA GGAGGCTCTG CTCCGCCTGC
 8751 TGCCTGCTGA GCTGCCTGCC AAGCGAGTCC GTGGGAAGGC CCGCCTCCCT
 8801 CCTGATGTCC TCAGATGGGT GGAGCTTGCT AAGCTGTATA GATCAATTGG
 8851 AGAATACGAC GTCCTCCGTG GGATTTTAC CAGTGAGATA GGAACAAAGC
 8901 AAATCACTCA GAGTGCATTA TTAGCAGAAG CCAGAAGTGA TTATTCGTAA
 8951 GCTGCTAACGC AGTATGATGA GGCTCTCAAT AAACAAGACT GGGTAGATGG
 9001 TGAGCCCACA GAAGCCGAGA AGGATTTTG GGAACCTGCA TCCCTTGACT
 9051 GTTACAACCA CCTTGCTGAG TGGAAATCAC TTGAATACTG TTCTACAGCC
 9101 AGTATAGACA GTGAGAACCC CCCAGACCTA AATAAAATCT GGAGTGAACC
 9151 ATTTTATCAG GAAACATATC TACCTTACAT GATCCGCAGC AAGCTGAAGC
 9201 TGCTGCTCCA GGGAGAGGCT GACCAAGTCCC TGCTGACATT TATTGACAAA
 9251 GCTATGCACG GGGAGCTCCA GAAGGCGATT CTAGAGCTTC ATTACAGTCA
 9301 AGAGCTGAGT CTGCTTACCC TCCTGCAAGA TGATGTTGAC AGAGCCAAAT
 9351 ATTACATTCA AAATGGCATT CAGAGTTTA TGCAGAATTA TTCTAGTATT
 9401 GATGTCCTCT TACACCAAAG TAGACTCACC AAATTGCAGT CTGTACAGGC
 9451 TTTAACAGAA ATTCAAGGAGT TCATCAGCTT TATAAGCAAA CAAGGCAATT
 9501 TATCATCTCA AGTTCCCCCTT AAGAGACTTC TGAACACCTG GACAAACAGA
 9551 TATCCAGATG CTAAAATGGA CCCAATGAAC ATCTGGGATG ACATCATCAC
 9601 AAATCGATGT TTCTTCTCA GCAAAATAGA GGAGAAGCTT ACCCCTCTTC
 9651 CAGAAGATAA TAGTATGAAT GTGGATCAAG ATGGAGACCC CAGTGACAGG
 9701 ATGGAAGTGC AAGAGCAGGA AGAAGATATC AGCTCCCTGA TCAGGAGTTG
 9751 CAAGTTTCC ATGAAAATGA AGATGATAGA CAGTGCCTGG AAGCAGAACAA
 9801 ATTTCTCACT TGCTATGAAA CTACTGAAGG AGCTGCATAA AGAGTCAAAA
 9851 ACCAGAGACG ATTGGCTGGT GAGCTGGGTG CAGAGCTACT GCCGCCTGAG
 9901 CCACTGCCGG AGCCGGTCCC AGGCTGCTC TGAGCAGGTG CTCACTGTGC
 9951 TGAAAACAGT CTCTTTGTTG GATGAGAACAC ACGTGTCAAG CTACTTAARC
 10001 AAAAATATTTC TGGCTTCCG TGACCAAGAC ATTCTCTTGG GTACAACCTTA
 10051 CAGGATCATA GCGAATGCTC TCAGCAGTGA GCCAGCCTGC CTTGCTGAAA

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Fig.10.

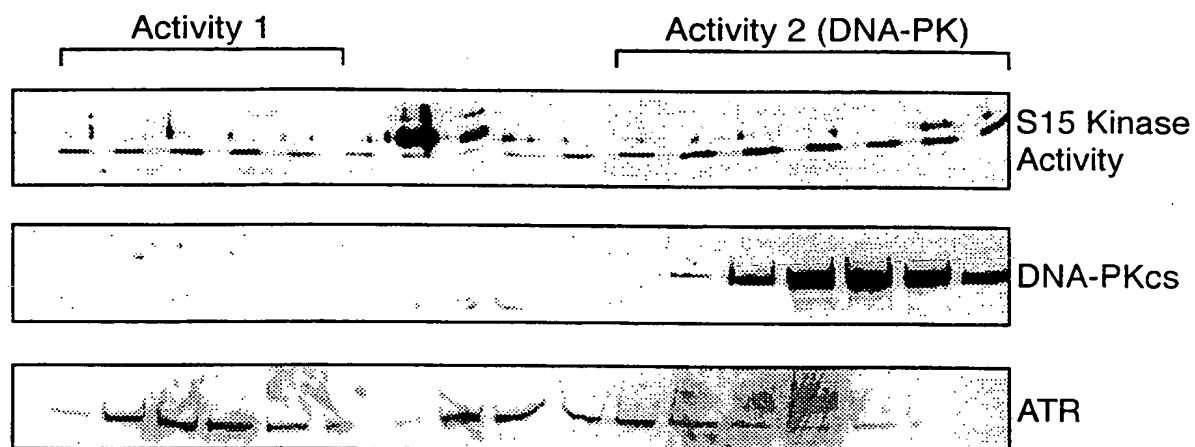


Fig.11.

